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Sequence Listing was accepted.

See attached Validation Report.

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217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=12; day=5; hr=8; min=36; sec=58; ms=570; ]

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Application No: 10537897 Version No: 2.0

Input Set:

Output Set:

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**Finished:** 2008-11-18 11:01:32.858  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 255 ms  
**Total Warnings:** 10  
**Total Errors:** 11  
**No. of SeqIDs Defined:** 52  
**Actual SeqID Count:** 52

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 257	Invalid sequence data feature in <221> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
E 257	Invalid sequence data feature in <221> in SEQ ID (7)
E 257	Invalid sequence data feature in <221> in SEQ ID (7)
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W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 257	Invalid sequence data feature in <221> in SEQ ID (8)
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W 213	Artificial or Unknown found in <213> in SEQ ID (9)
E 257	Invalid sequence data feature in <221> in SEQ ID (9)
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W 402	Undefined organism found in <213> in SEQ ID (24)
W 402	Undefined organism found in <213> in SEQ ID (25)
E 257	Invalid sequence data feature in <221> in SEQ ID (51)

**Input Set:**

**Output Set:**

**Started:** 2008-11-18 11:01:29.603  
**Finished:** 2008-11-18 11:01:32.858  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 255 ms  
**Total Warnings:** 10  
**Total Errors:** 11  
**No. of SeqIDs Defined:** 52  
**Actual SeqID Count:** 52

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (52)

# SEQUENCE LISTING

<110> MOLINERO, ANA ISABEL SANZ

<120> PLANTS HAVING MODIFIED GROWTH CHARACTERISTICS AND A METHOD FOR  
MAKING THE SAME

<130> 4982-5

<140> 10537897

<141> 2005-06-07

<150> PCT/EP03/51104

<151> 2003-12-24

<150> EP 02080654.3

<151> 2002-12-24

<160> 52

<170> PatentIn version 3.5

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<211> 692

<212> DNA

<213> Arabidopsis thaliana

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<212> PRT

<213> Arabidopsis thaliana

<400> 2

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20 25 30

Lys Gly Lys Arg Ser Lys Arg Ser Arg Ser Asp Phe His His Gln Asn  
35 40 45

Leu Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg  
50 55 60

Asp Asn Arg Gln Pro Pro Pro Pro Pro Ala Val Glu Lys Leu Ser Tyr  
65 70 75 80

Lys Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly  
85 90 95

Gly His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly  
100 105 110

Gly Gly Asp Asp His Ser Thr Ser Ser Ala Thr Thr Thr Ser Ala Val  
115 120 125

Thr Thr Gly Ser Gly Lys Ser His Val Cys Thr Ile Cys Asn Lys Ser  
130 135 140

Phe Pro Ser Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu  
145 150 155 160

Gly Asn Asn Asn Ile Asn Thr Ser Ser Val Ser Asn Ser Glu Gly Ala  
165 170 175

Gly Ser Thr Ser His Val Ser Ser Ser His Arg Gly Phe Asp Leu Asn  
180 185 190

Ile Pro Pro Ile Pro Glu Phe Ser Met Val Asn Gly Asp Asp Glu Val  
195 200 205

Met Ser Pro Met Pro Ala Lys Lys Pro Arg Phe Asp Phe Pro Val Lys  
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Leu Gln Leu

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<211> 50

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<223> Description of Artificial Sequence: Synthetic primer

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<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

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<210> 6

<211> 6

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD\_RES

<222> (3)..(3)

<223> Met or Trp

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<210> 7

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic peptide

<220>

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<220>

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<222> (5)..(5)

<223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Arg, Thr,  
Val, Trp or Tyr

<220>

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<222> (6)..(6)

<223> Variable amino acid or not present

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1 5

<210> 8

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic peptide

<220>

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<222> (3)..(3)

<223> May or may not be present

<220>

<221> MOD\_RES

<222> (6)..(6)

<223> Variable amino acid

<400> 8

Lys Arg Ser Lys Arg Xaa Arg

1 5

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<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide

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<213> Datisca glomerata

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aagcaacgac ttccgctacc aaagtcagtt ataagtgtc tgtgtgcat aaggcctttt 360  
cgtcttatca ggctttgggt gggcacaagg ccagccacag aaagctcgct ggcggaag 420  
atcaatcgac ttcccttgcc accacgaatt cagccaccgt cactaccacc acagcctccg 480  
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<210> 11

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<212> PRT

<213> *Datisca glomerata*

<400> 11

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His Tyr Asp Asp Pro Ser Leu Asn Tyr Leu Glu Pro Trp Thr Lys Arg
          20          25          30

```

```

Lys Arg Ser Lys Arg Thr Arg Leu Asp Ser Pro His Thr Glu Glu Glu
          35          40          45

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```

Tyr Leu Ala Phe Cys Leu Ile Met Leu Ala Arg Gly Arg Val Ala Ser
          50          55          60

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Ala Asn Arg Arg Asp Ser Gln Ser Ser Ile Gln Ile Gln Pro Glu Ala
          65          70          75          80

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```

Thr Thr Ser Ala Thr Lys Val Ser Tyr Lys Cys Ser Val Cys Asp Lys
          85          90          95

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Ala Phe Ser Ser Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg
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Lys Leu Ala Gly Gly Glu Asp Gln Ser Thr Ser Phe Ala Thr Thr Asn
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Ser Ala Thr Val Thr Thr Thr Thr Ala Ser Gly Gly Gly Gly Arg Ser
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His Glu Cys Ser Ile Cys His Lys Ser Phe Pro Thr Gly Gln Ala Leu  
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Gly Gly His Lys Arg Cys His Tyr Glu Gly Ser Ile Gly Gly Asn Ser  
165 170 175

Ile His His His Asn Asn Thr Thr Asn Ser Gly Ser Asn Gly Gly Met  
180 185 190

Ser Met Thr Ser Glu Val Gly Ser Thr His Thr Val Ser His Ser His  
195 200 205

Arg Asp Phe Asp Leu Asn Ile Pro Ala Leu Pro Glu Phe Arg Ser Asn  
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Phe Phe Ile Ser Gly Asp Asp Glu Val Glu Ser Pro His Pro Ala Lys  
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Lys Pro Arg Ile Leu Met Lys  
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<210> 12

<211> 996

<212> DNA

<213> Glycine max

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cttctgaaga agagtacctc gccctctgcc tcatcatgct cgctcgcggc ggcaccacca 240

ccgtcaacaa ccgccacgtc agccctccgc cgctacagcc acagccacag ccgacaccag 300

atccttcac caagctcagt taaaaatgct ccgtttgcga caagagcttc ccctcttacc 360

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gttgtcacta cgaaggtaac ggtaacggaa ataacaacaa cagtaacagc gttgtcaccg 600

tgcctcggga aggcgtgggc tccaccaca ctgtcagtca cggccaccac cgcgacttcg 660

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<210> 13

<211> 240

<212> PRT

<213> Glycine max

<400> 13

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Pro Phe Asp Asp Pro Thr Ile Pro Trp Ala Lys Arg Lys Arg Ser Lys  
 20 25 30

Arg Ser Arg Asp His Pro Ser Glu Glu Glu Tyr Leu Ala Leu Cys Leu  
 35 40 45

Ile Met Leu Ala Arg Gly Gly Thr Thr Thr Val Asn Asn Arg His Val  
 50 55 60

Ser Pro Pro Pro Leu Gln Pro Gln Pro Gln Pro Thr Pro Asp Pro Ser  
 65 70 75 80

Thr Lys Leu Ser Tyr Lys Cys Ser Val Cys Asp Lys Ser Phe Pro Ser  
 85 90 95

Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg Lys Leu Ala Gly  
 100 105 110

Ala Ala Glu Asp Gln Pro Pro Ser Thr Thr Thr Ser Ser Ala Ala Ala  
 115 120 125

Thr Ser Ser Ala Ser Gly Gly Lys Ala His Glu Cys Ser Ile Cys His  
 130 135 140

Lys Ser Phe Pro Thr Gly Gln Ala Leu Gly Gly His Lys Arg Cys His

145 150 155 160

Tyr Glu Gly Asn Gly Asn Gly Asn Asn Asn Asn Ser Asn Ser Val Val  
165 170 175

Thr Val Ala Ser Glu Gly Val Gly Ser Thr His Thr Val Ser His Gly  
180 185 190

His His Arg Asp Phe Asp Leu Asn Ile Pro Ala Phe Pro Asp Phe Ser  
195 200 205

Thr Lys Val Gly Glu Asp Glu Val Glu Ser Pro His Pro Val Met Lys  
210 215 220

Lys Pro Arg Leu Phe Val Ile Pro Lys Ile Glu Ile Pro Gln Phe Gln  
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 <212> PRT  
 <213> Medicago sativa

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 35 40 45

Glu Glu Tyr Leu Ala Leu Cys Leu Ile Met Leu Ala Arg Ser Gly Asn  
 50 55 60

Asn Asn Asp Lys Lys Ser Asp Ser Val Ala Thr Pro Leu Thr Thr Val  
 65 70 75 80

Lys Leu Ser His Lys Cys Ser Val Cys Asn Lys Ala Phe Ser Ser Tyr  
 85 90 95

Gln Ala Leu Gly Gly His Lys Ala Ser His Arg Lys Ala Val Met Ser  
 100 105 110

Ala Thr Thr Ala Glu Asp Gln Ile Thr Thr Thr Ser Ser Ala Val Thr  
 115 120 125

Thr Ser Ser Ala Ser Asn Gly Lys Asn Lys Thr His Glu Cys Ser Ile  
 130 135 140

Cys His Lys Ser Phe Pro Thr Gly Gln Ala Leu Gly Gly His Lys Arg  
 145 150 155 160

Cys His Tyr Glu Gly Ser Val Gly Ala Gly Ala Gly Ala Gly Ser Asn  
 165 170 175

Ala Val Thr Ala Ser Glu Gly Val Gly Leu Ser His Ser His His Arg  
180 185 190

Asp Phe Asp Leu Asn Leu Pro Ala Phe Pro Asp Phe Ser Lys Lys Phe  
195 200 205

Phe Val Asp Asp Glu Val Phe Ser Pro Leu Pro Ala Ala Lys Lys Pro  
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Cys Leu Phe Lys Leu Glu Ile Pro Ser His Tyr  
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<212> DNA

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<400> 17

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